

PRIMARY HIV-1 ISOLATE

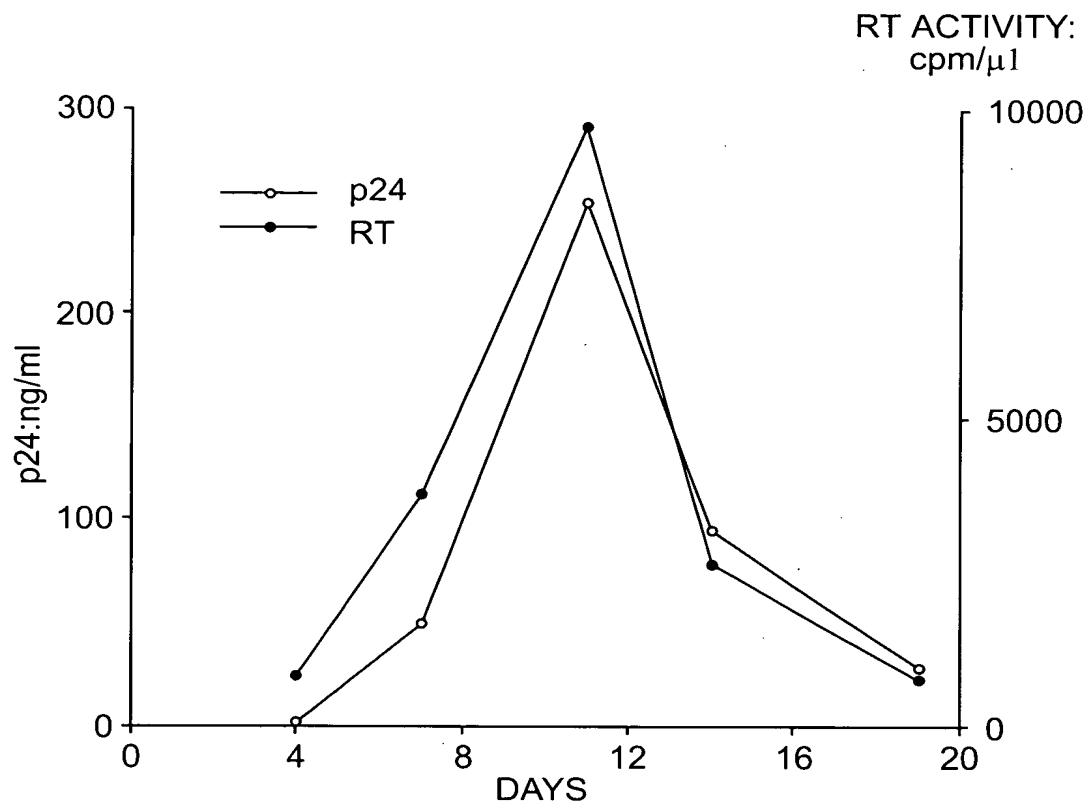


FIG. 1A

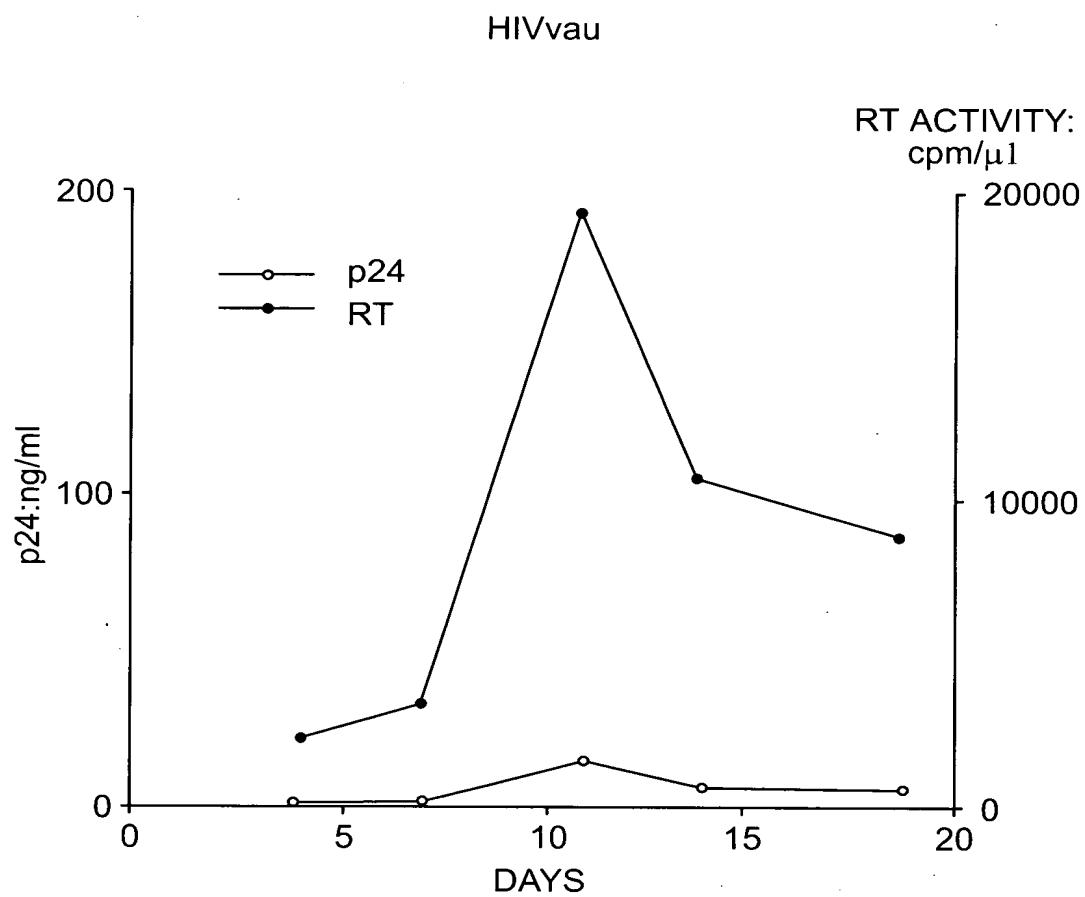


FIG. 1B

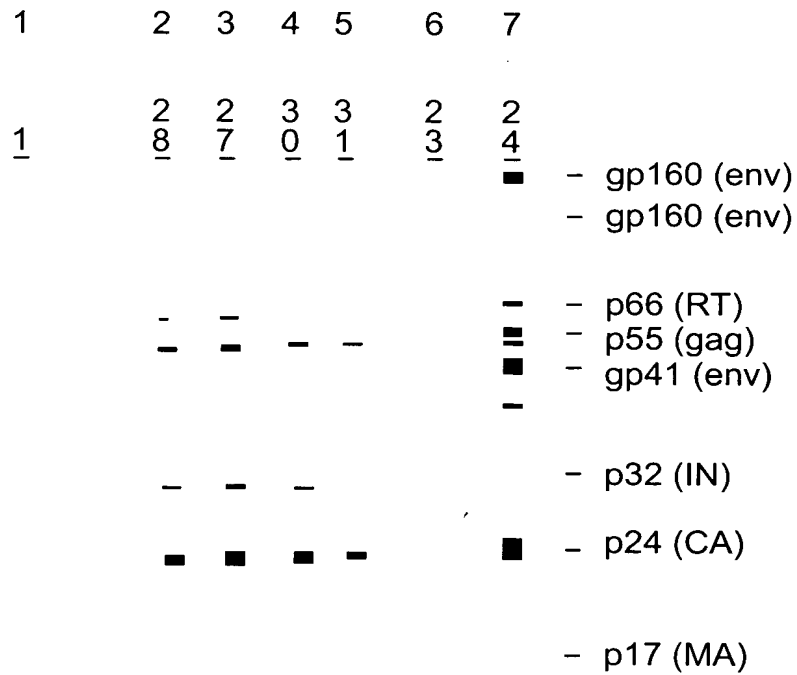


FIG. 2

		SIGNAL PEPTIDE		
VAU	1	..MTAIMKAMGKRNRLGIWCLILALIIPCL	SCNQLYATVYSGVPVWEDA	48
		... : : : : : : : : : : : : :	
LAI	1	MRVKEKYQHLWRWGKKG..TLLGILMICS	ATEKLWVTVYYGVPVWKEA	48
VAU	49	KPTLFCASDANLTSTEQHNIWATQACVPTDPS	PNEYELKNVTGKFNIWKN	98
		..	: . :	
LAI	49	TTTLFCASDAKAYDTEVHNWATHACVPTDPNP	QEVVLNVNVTENFNMWKN	98
VAU	99	YIVDQMHEDIIDLWDQSLKPCVQMTFLCVQM	NCTDIKNSINTNSPLNSN	148
		: : :	: . : :	
LAI	99	DMVEQMHEDIISLWDQSLKPCVKLTPLCVSLK	CTDLGNATNTNSSNTNSS	148
VAU	149	NTK.....EVKQCDFNVTTVLKDKQEKQ	ALFYVTDLVKINATSNETMY	192
		... : . . : : : :	: : : . : : .	
LAI	149	SGEMMEKGEIKNCSFNISTSIRGKVQKEYA	FFYKLDIIPID..NDTTSY	196

FIG. 3A

VAU	193	RLINCNSTTIRQACPKVSFEPIPIHYCAPAGCAIFKCNETGFNGTGLCKN	242
		
LAI	193	TLTSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTN	246
VAU	243	VTVVTCTHGIKPTVSTQLILNGTLSKGNITIMGKNISDSGENILITLNTN	292
		.. : . : : : :: .	
LAI	247	VSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS	296
		V3 LOOP	
VAU	293	ITIA CERPGNQTIQKIMAGPMAWYSMALSN TKGDTRAAYCNYSATDWNKA	342
		:. : :	
LAI	297	VEINCTRPNNNTRKSIRIQRGPGRAFTIGKIGNMRQAHCNISRAKWNAT	346
VAU	343	LKNITERYLELVEYNQTDVTMKFGNHSGEDAEVTNFFFNCHGEFFYCNTN	392
	 : . : : . : : :.. ..	
LAI	347	LKQIASKLREQFGNNKTII...FKQSSGGDPEIVTHSFNCGGEFFYCNST	393
VAU	393	RLFNHTFSCCKNMTNNKINCTNISNNSNGTQAI..PCRLRQVVRDWMRGG	440
		. : .. : : .: :.. : :.. .	
LAI	394	QLFNSTWF.....NSTWSTEGSNNTGSDTITLPCRIKQFINMWQEVG	436

FIG. 3B

IMMUNODOMINANT EPITOPE

FIG. 3C

VAU	640	LTWQQWDQQINNVSSFIYEKIQEAQEQQEKNEKELLELDEWASIWNWLDI	689
LAI	631	MTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNI	680
VAU	690	TKWLWYIKIAIIIVGALIGVRVVMIVLNLVKNIRQGYQPLSLQIPIQQQA	739
LAI	681	TNWLWYIKIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPR	730
VAU	740	EVGTPGGTGEGGGDEDRRRWTPLPQGFLHLLYTDLRTIILWIYHLLSNLA	789
LAI	731	GPDRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRLSLCLFSYHRLRDLL	780
VAU	790	SEIQKLIRHLGLGLWIIIGORTIEACRLFKAI IQYWLQELQTSATNLDDTV	839
LAI	781	LIVTRIVE.....LLGRRGWEALKYWWNLLQYWSQELKNSAVSLNAT	823
VAU	840	AVAVANWTDSTILGIQSIGRGILNIPRRIRQGLERLLL	877
LAI	824	AIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL	861

FIG. 3D

HIV-1lai	RILAVERYLKDQQLLGIWGCSGKLIC
HIV-1Z321	-----I--
HIV-1eli	-----H--
HIV-1JRCSF	-V-----M-----
HIV-1WMJ	-V-----R-----
HIV-1NDK	-V-----R-----RH--
HIV-1mal	-V-----Q--R--M-----H--
SIVCPZGAB	-L-----Q---I--L-----AV-
 vau	 -L--L-TFIQN---NL---KNR---
mvp5180	-LQ-L-TLIQN--R-NL---K-----
ant70	-L--L-TL-QN---SL---K---V-
 HIV-2rod	 -VT-I-K--Q--AR-NS---AFRQV-
HIV-2D194	-VT-I-K-----AQ-NS---AFRQV-

FIG. 4

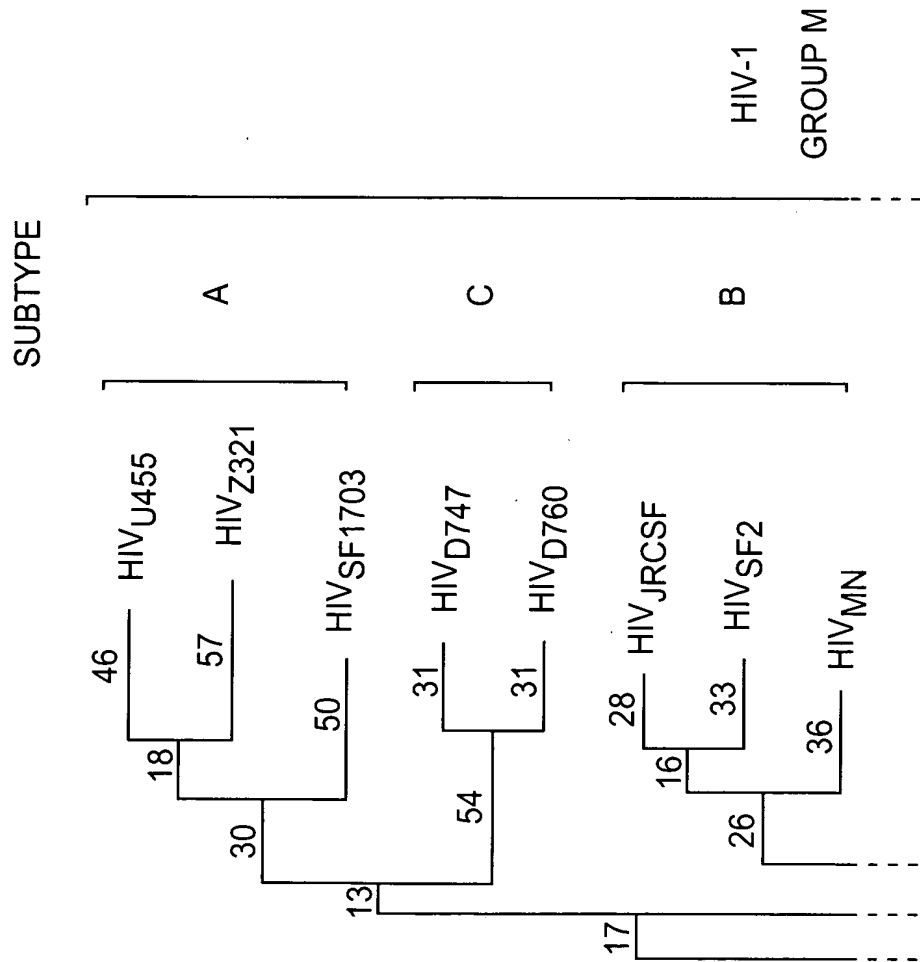
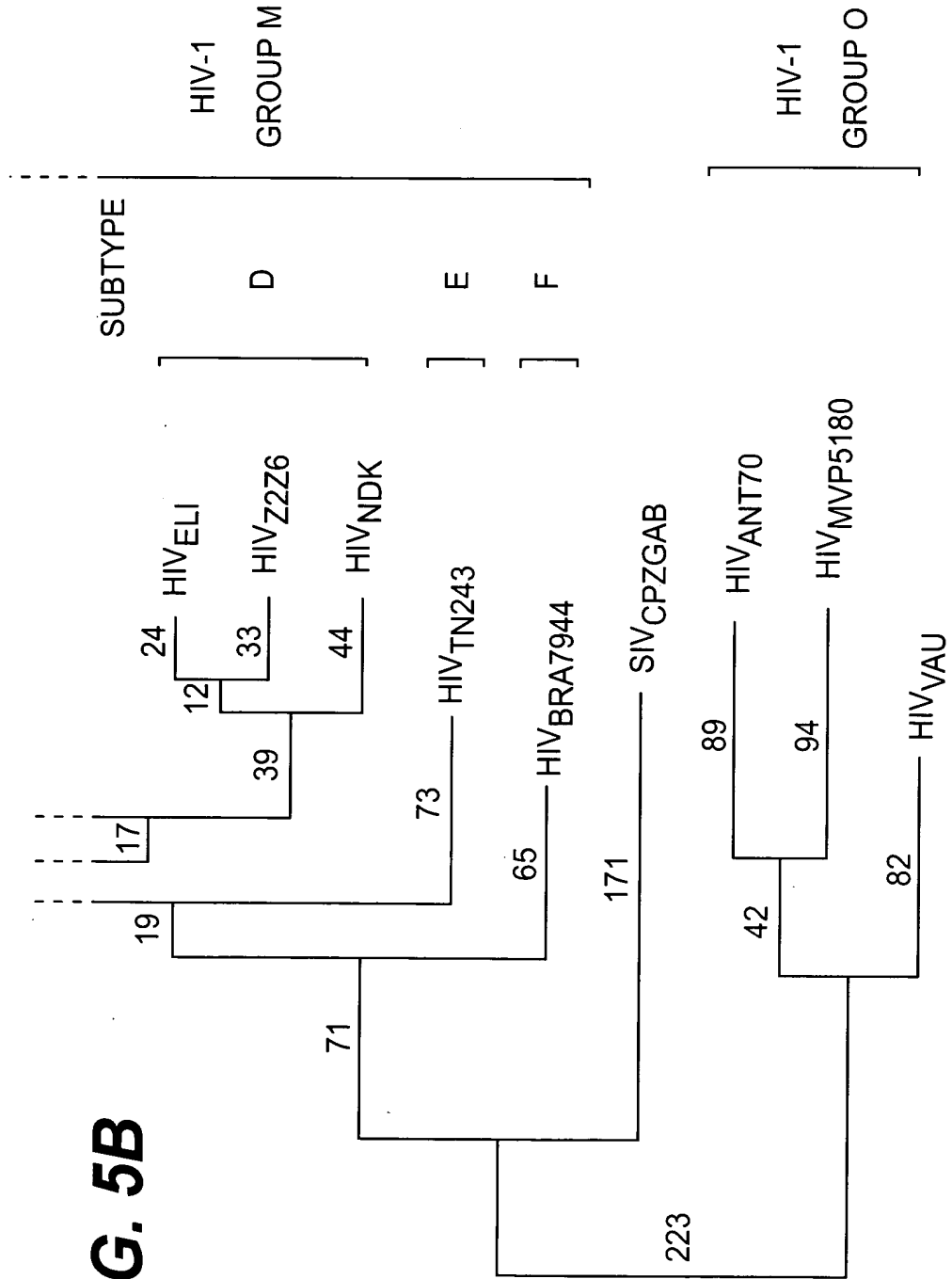


FIG. 5A

FIG. 5B



DNA SEQUENCE 2631 B.P. ATGACAGCGATT ... CGACTCCTGTGTTA LINEAR

	10	20	30	40	50		60	70	80	90	100
1	ATGACAGCGA	TTATGAAAGC	AATGGGGAAG	AGGAACAGGA	AGTTAGGGAT		CTGGTGGCTTG	ATTTTGGCTT	TGATAATCCC	ATGTTTGAGC	TGTACCAAC
101	TATATGCCAC	AGTCTATTCT	GGGTACCTG	TATGGGAAGA	TGCAAAACCA		ACATTGTCTT	GTGCTTCAGA	TGCTTAACITG	ACAGCACTG	AACAGCATAA
201	TATTTGGGCA	ACACAAGCCT	GTGTTCCCA	AGACCCAGT	CCAAATGAAT		ATGAGGTAAA	AAATGTGACA	GGTAAATTC	ATATATGGAA	AAATATATATA
301	GTAGACCAAA	TGCACGAAGA	CATTATAGAT	TTGTGGGACC	AGAGTTTAAA		ACCTTGTGTT	CAAAATGACTT	TCTTGTGTT	ACAAATGAAT	TGTACAGATA
401	TCAAAAATAG	TATTAATACC	ACAAACAGTC	CCTTAAACTC	AAACAATACA		AAAGAGGTGA	AAACAGTGTGA	CTTTAATGTA	ACTACAGTGC	TCAAAGACAA
501	ACAGGAGAAA	AAACAGGCTC	TATTTATATG	GACAGATTGG	GTTAAGATT		ACGCCACATC	AAATGAAACA	ATGTATAGAT	TAATTAATG	TAACCTCCACA
601	ACCATCAGGC	AGCCTGTCC	AAAGTATCT	TTTGAGCCCC	TTCCCATACA		CTATTGTGCT	CCAGCGGGAT	GTGCCATCTT	TAAGTGAAT	GAACAGGAT
701	TAAATGGAAC	AGTCTCTGT	AAAACGTTA	CAGTAGTTAC	TTGTACACAT		GGCATCAAA	CAACAGTAAG	TACCCAACTA	ATACTAAATG	GGACACTCTC
801	TAAAGGAAAT	ATAACAATCA	TGGGAAAGAA	TATTTACAGC	AGTGGGGAGA		ACATCCTAAT	AACCTTAAT	ACTAATATAA	CAATAGCATG	TGAGAGACCA
901	GGAAATCAGA	CAATACAAA	GATAATGGCA	GGTCAATGG	CTTGTACAG		CATGGCCCTT	AGTAATACAA	AGGGGATAC	AAGGCAGCT	TATTTAAT
1001	ATAGTGGCAC	TGACTGGAC	AAACCTTAA	AAAACATAAC	TGAAGATAT		TTAGAACTTG	TAGAATATA	TCAAACTGAT	GTTACCATGA	AATTCGGTAA
1101	TCACAGTGGT	GAAGATGCAG	AGTAAACAAA	TTTTCTTTTT	AACGTGATG		GAGAACTCTT	TTATTGTAAC	ACAAATCGGC	TGTTAATCA	TACCTTTTCC
1201	TGCAAGAGA	ATATGACCAA	TAAACAAGTC	AATTGTACTA	ATATTAGCAA		TAATAGCAAT	GGCACTCAGG	CAATACCTTG	CAGGTTGAGA	CAAGTAGTAA
1301	GGGACTGGAT	GAGGGGAGGA	TGGGACTTTT	ATGCACCTCC	CATCCAGGA		AACCTAGTAT	GCAGGTCAAA	CATAACTGGA	ATGATTCTAC	AATTGGACAC
1401	GCCATGGAAT	AAAACACATC	CTAACAGCAC	CACCTTAGA	CCAGGAGGGG		GAGATATGAA	AGATATATGG	AGAACTCAAT	TGTTCAAATA	TAAAGTAGTA
1501	AGAGTAAAC	CTTTTAGTGT	AGCACCAACA	AAAATTGCAA	GGCCAATAT		AGGAACTAGA	TCTCATAGAG	AGAAAAGAGC	AGCAGGTTTG	GCAATGCTAT
1601	TCTTGGGAT	TCTAAGTGA	GCAGGAAGCA	CTATGGGGC	AGCGGCAACA		CGCTGACCG	TACGGACCCA	GCATCTGATA	AAGGTATAG	TGCAACAGCA
1701	GGATAACCTG	CTAAGAGCAA	TACAGGCCCA	GCACACTTG	CTGAGGCCAT		CTGTATGGGG	TATTAGACAA	CTCCGAGCTC	GCCTGCTAGC	CTTAGAAAAC
1801	TTTATACAGA	ATCAGCAACT	CCTTAACCTG	TGGGGCTGCA	AGAATAGACT		AATCTGCTAC	ACATCAGTAA	AGTGGGAATA	AACATGGGGA	GGAGATAATG
1901	AATCAATTG	GGATGAGTTA	ACATGGCAGC	AGTGGGATCA	ACAGATAAAC		AACGTAAGCT	CCTTCATATA	TGAAAAATA	CAAGAGGCAC	AAGAAACAACA
2001	GGAGAAAAT	GAGAAAGAA	TGCTGGAGTT	AGATCAATGG	GCCTCTATTT		GGAAATGGCT	TGACATAACT	AAATGGTTCT	GGTATATATA	AATAGCTATA
2101	ATCATAGTAG	GAGCACTAAT	AGGTGTAAGA	GTAGTTATGA	TAGTACTTAA		TCTAGTAAAG	AACATTAGGC	AGGATATCA	ACCCCTCTCG	TTACAGATCC
2201	CCATCCACAA	ACAAGCGGAA	GTAGGAACGC	CAGGAGGAAC	AGGAGAGGA		GGTGGAGACG	AAGACAGCGG	CAGGTGGACT	CCATTGCCGC	AAGGTTCTTT
2301	GCATCTGTTG	TACACGGACC	TCAGGACAA	AATCTTGTTG	ATTACCAACC		TCTTGAGCAA	CTTAGCCCTCA	GAGATCCAGA	AGTTGATCAG	ACACCTGGGA
2401	CTTGACTAT	GGATCATAGG	GCAGAGGACA	ATTGAAGCTT	GCAGACTCTT		TAAAGCTATA	ATACAATACT	GGCTACAAGA	ATTGCAAACT	AGTGCTACAA
2501	ATCTACTAGA	TACTGTTGCA	GTGGCAGTTG	CTAATTGGAC	TGACACACA		ATCTTAGGCA	TACAAAGCAT	AGGGAGAGGG	ATTCTTAACA	TACCAAGAAG
2601	GATTAGACAG	GGCCTTGAC	GACTCCTGTT	A							

FIG. 6

```

1 GCAGAGACAG GACAGGAAAC TGCCTACTTC CTGTTAAAT TAGCAGCAAG ATGGCCTATT AAAATACTAC ATACAGACAA 80
81 TGGGCCTAAC TTTACAAGTG CAGCCATGAA AGCTGCATGT TGGTGGACAA ACATACAACA TGAGTTTGGG ATACCATACA
161 ATCCACAAAG TCAAGGAGTA GTAGAAGCCA GTACAAGGA ATTAAATCA ATCATACAGG TGAGGGACCA AGCAGAGCAC
241 TTAAGGACAG CAGTACAAAT GGCAGTATT GTTCACAAT TTAAAGAAA AGGGGGGATT GGGGGGTACA CTGCAGGAGA
321 GAGATTAAAT GACATATTAG CATCACAAAT ACAACAACA GAACTACAAA AACAAATTT AAAAATTCAA AATTTTCGGG
401 TCTATTACAG AGACAGCAGA GACCCTATTT GGAAGGACC GGCACAGCTC CTG
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80
```

FIG. 7

	<u>GAG REGION</u>									
	#	#	#	#	#	#	#	#	#	#
DUR	qgqmvhqalsprtlnawvkaveekafnpeiipmfmalsegavpydinvmalnaigghqgal									
ANT	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----
MVP	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----
LAI	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----
MAL	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----
CPZ	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----	-----i-----

FIG. 8A

	#	#	#
DUR			vgdiyrkwivlglnkmvkmypsvsildirgqpkpfrdyvdrfyktlrae
ANT			-----k-----
MVP			-----
LAI			--e--kr--i-----i-r--t-----
MAL			-----kr--i-----i-r-----f-----
CPZ			---v--r-vi-----v-r--c-----

HIV1-M / HIV1-O DISCRIMINATING POSITIONS : #

HYPERVARIABLE REGIONS : ||||

FIG. 8C

REGION OF THE V3 LOOP OF GP120

----	YK	---	QRTG	---	O	LY	---	THR	I	DI	----	MAD																												
C	T	R	P	N	N	T	R	K	S	I	R	I	Q	R	G	P	A	F	V	T	I	G	K	I	G	N	M	R	Q	A	H	C	LAI							
---	---	---	NR	S	---	---	---	H	---	---	---	TKQ	I	DI	---	OYI																								
-	A	-	YQ	---	Q	R	T	P	-	L	-	Q	S	L	Y	-	TR	S	R	S	I	I	G	---	ELI															
---	G	---	---	---	RG	I	H	F	---	---	---	Q	A	L	Y	-	T	-	V	D	I	-	R	Y	MAL															
-	S	-	Y	-	TR	K	N	I	R	R	Y	S	I	-	S	-	Q	A	F	Y	V	T	---	I	DI	-	Q	---	455											
-	H	-	G	---	GE	---	VQI	---	MT	F	Y	N	---	ENV	V	DT	---	S	Y	---	CPZ																			
-	E	-	Q	I	DI	QE	MRI	---	M	-	W	Y	S	M	G	---	G	T	A	---	S	S	---	Y	ANT															
-	I	-	E	G	I	A	E	V	Q	D	-	Y	T	---	MR	W	R	S	M	---	T	L	I	R	S	N	N	T	S	-	V	-	Y	MVP						
-	E	-	G	-	Q	T	I	Q	-	MA	---	M	-	W	Y	S	M	A	L	S	N	T	K	-	D	T	---	A	-	Y	---	VAU								
-	V	-	G	-	S	-	V	-	E	-	K	---	M	-	W	Y	S	M	Q	-	E	R	E	G	K	G	A	N	S	-	T	-	F	DUR						
C	*	R	*	*	*	*	I	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	HIV-O	CONSENSUS				
C	V	R	P	G	N	N	S	V	K	E	I	K	I	---	G	P	---	M	A	W	Y	S	M	Q	I	E	R	E	G	K	G	A	N	S	R	T	A	F	C	DUR

FIG. 9A

IMMUNODOMINANT REGION OF GP41
[~~~~~]

[=====]

MAD	-V-----Q-----H---T---S---
LAI	RILAVERYLKDQQLLGIWGSGKLICTTAVPWNASWS
OYI	-V-----T-----
ELI	-----H---N---S---
MAL	-V-----Q-R---M---H---F---S---
455	-V-----Q-----T---S---
CPZ	-L-----Q---I---L-----AV-Y-T---N---P

ANT	-L--L-TL-QN-----SL---K---V-Y-S-K--RT-I
MVP	-LQ-L-TLIQN--R-NL--K-----Y-S-K--RT-I
VAU	-L--L-TFIQN-----NL---KNR---Y-S-K--KT-G
DUR	-L--L-TLMQN-----NL---R--A--Y-S-Q--ET-G

HIV-0 CONSENSUS RL*ALET**QNQQ*L*WGC*****CYTSV*WN*TW*

DUR	RLLALETLMQNQQQLLN <u>WG</u> CRGKAICYTSVQWNETWG
-----	--

[_____]

...

FIG. 9B

CAGGGACAAATGGTACATCAGGCCATCTCCCCAGAACTTTATATGTATGGGTAAGGCA
GTAGAAGAAAAGGCCCTTTAACCTGAAATATCCCTATGTTTATGGCACTATCAGAAGGA
GCTGTTCCCTATGATATCAATGTTATGCTAAATGCCATAGGAGCACCAAGGGGCTTTA
CAAGTATTAAAGAAGTAATCAATGATGAAGCAGCAGACTGGGATAGAGCTACCCACAA
CAGGCAGGCCCGTTACCAACAGGGCAGATAAGGGAACCAACAGGAAGTGACATTGCTGGA
ACAACTAGCACACAGCAAGAGCAATCTCTGGACTACTAGGCGAGGTAAACCCTATCCCA
GTTGGACACATCTATAGGAAATGGATAGTGTGGGTCTAAACAAAATGGTAAAAATGTAT
AGTCCAGTGAGCATCTTAGATATTAGGCGAGGACCAAAAGAACCATTTAGAGATTATGTA
GACAGGTTCTACAAAACATTAAAGAGCTGAGCAG

GAG REGION OF HIV1-0 DUR STRAIN: 513 BASE PAIRS

= SEQ ID N° 9

FIG. 10A

QQQMVHQALSPRTLNAWVKAVEEKAENPEIIPMFMAISEGAVPYDINVMLNAIGHQCAL
QVLKEVINDEAADWDRAHPQQAGPLPPGQIREPTGSDIAGTTSTQQEQILWTTAGNPIP
VGDIYRKWIVLGLNKMVKMYSVPSILDIRQGPKEPFRDYVDREYKTLRAEQ

GAG REGION OF HIV1-0 VIRUS DUR STRAIN: 171 AMINO ACIDS

FIG. 10B

ATTCCAATACACTATTGTGCTCCAGCAGGATATGCTATCTTTAAATGCAACACGAGGAG
TTTTACTGGAAGAGCCCATGTAAACAATTTCACTAGTAGTTACCTGTACACAGGGTATCAAG
CCAACAGTAAGCACTCATCTAATATTCAATGGGACAACTCTCTGAAAGAAAAATAAGAATT
ATGGGAAAGAACATCTCGAGCAACTCAGGTAATATCCTAGTGACCCCTAAATTTACTATA
AACATGACCTGTGTGAGGCCAGGAATAATTCAGTACAGGAGATAAAAATAGGTCCAATG
GCTTGGTACAGTATGCAAAATTGAGCGAGAGGAAAAAGGACAAATTCAGAACACAGCTTTT
TGTAACCTATAATGCCACGGACTGGAGAAAAACCTTGCAAGGATAGCTGAAAGGTATTTA
GAACTGTAAATAAAACAAGTCCGACTGAAATAATGTTCAATAAAAGCAATGGTGGAGAT
GCAGAAATAACCCGTTTGCAATTTTAACTGTCATGGAGAATTCTTT

V3 LOOP OF GP120 DUR STRAIN: 525 BASE PAIRS

= SEQ ID N° 10

FIG. 11A

IPIHYCAPAGYAIKCNNEEFTKGPCNNISWWTCTQGIKPTVSTHLIFNGTISERKIRI
MGNISSNSGNILVTLNSTINMTCVRPGNNSVQEIKIGPMAWYSMQIEREGKANSRTAF
CTYNATDWRKTLQIAERYLELVNKTSPTEIMFNKNSGGDAEITRLHFNSCGEFF

V3 LOOP OF GP120 DUR STRAIN: 175 AMINO ACIDS

FIG. 11B

ATAGTGCAACAGCAGGACAACCTGCTGAGAGCAATAACAGGCCCCAGCAACATCTGCTGAGG
TTATCTGTATGGGTATTAGACAACCTCCGAGCTCGCTGTAGCCTTAGAAACCCCTTATG
CAGAAATCAGCAACTCCTAAACCTGTGGGTTAGAGGAAAAGCAATCTGCTACACATCA
GTACAATGGAATGAACATGGGGAGGAAATGACTCAATTGGGACAGGTTAACATGGCAG
CAATGGGATCAACAGATAGCCAATGTAAGCTCTTTTATATATGACAAAATACAGAAGCA
CAAGAACACAA

DNA SEQUENCE OF THE IMMUNODOMINANT REGION OF GP41 OF
HIV1-O DUR: 312 BASE PAIRS

= SEQ ID N° 11

FIG. 12A

IVQQQDNLLRAIQAAQQLRLRLSVWGIRQLRARLLAETLMQNQQLNLLWGCGRKAICYTS
VQWNETWGGNDSIWDRLTWQQDQQIANVSSFTYDKIQEAQEQQ

DNA SEQUENCE OF THE IMMUNODOMINANT REGION OF GP41 OF
HIV1-O DUR - PREDICTED PROTEIN: 104 AMINO ACIDS

FIG. 12B

SPECIFIC PRIMERS OF THE HIV-O TYPE

DUR V3a	ATT-CCA-ATA-CAC-TAT-TGT-GCT-CCA-3'
DUR V3r	AAA-GAA-TTC-TCC-ATG-ACT-GTT-AAA-3'
DUR 41a	GGT-ATA-GTG-CAA-CAG-CAG-GAC-AAC-3'
DUR 41r	AGA-GGC-CCA-TTC-ATC-TAA-CTC-3'

FIG. 13A

POSITIONS OF THE PRIMERS:

IN HIV MVP5180

dur V3a	6896 TO 6919
dur V3r	7400 TO 7423
dur 41a	7934 TO 7957
dur 41r	8292 TO 8302

IN HIV ANT70

dur V3a	6896 TO 6920
dur V3r	7392 TO 7415
dur 41a	7917 TO 7940
dur 41r	8256 TO 8276

IN HIV1 VAU

dur V3a	640 TO 663
dur V3r	1138 TO 1161
dur 41a	1684 TO 1707
dur 41r	2026 TO 2046

FIG. 13B

V3	
HIV1-M CONSENSUS	NEGATIVE
HIV1-M MAL (AFRICAN)	NEGATIVE
HIV1-M CTV-CPZ (CHIMPANZEE)	NEGATIVE
HIV1-O MVP5180	NEGATIVE
HIV1-O ANT70	POSITIVE

FIG. 14A

GP41	
HIV1-M CONSENSUS:	
-PASTEUR STANDARD	NEGATIVE
-INNOGENETICS RIGHT-EXTENDED	WEAK POSITIVE
HIV1-O MVP5180:	
-INNOGENETICS	NEGATIVE
-BEHRING LEFT-EXTENDED	POSITIVE
HIV1-O VAU	POSITIVE

FIG. 14B

NUCLEOTIDE COMPARISONS
 EXPRESSED AS PERCENTAGE DIFFERENCE

GP41 (OUT OF 330 BASES)

LAI	0							
MAL	11	0						
CPZ	33	31	0					
MVP5180	39	38	38	0				
ANT70	36	39	37	15	0			
VAU	39	38	38	14	14	0		
DUR	38	36	37	13	15	11	0	
	LAI	MAL	CPZ	MVP	ANT	VAU	DUR	
				5180	70			

FIG. 15A

V3 (OUT OF 558 BASES)

LAI	0						
MAL	19	0					
CPZ	37	34	0				
MVP5180	46	43	45	0			
ANT70	45	44	43	23	0		
VAU	44	41	41	24	24	0	
DUR	46	43	42	25	22	24	0
	LAI	MAL	CPZ	MVP	ANT	VAU	DUR
				5180	70		

FIG. 15B

GAG (OUT OF 520 BASES)

LAI	0						
MAL	9	0					
CPZ	21	25	0				
MVP5180	24	26	25	0			
ANT70	25	25	24	10	0		
DUR	25	26	25	9	10	0	
	LAI	MAL	CPZ	MVP	ANT	DUR	
				5180	70		

FIG. 15C

FIG. 16A

V3 (OUT OF 186 AMINO ACIDS)

LAI	0						
MAL	31	0					
CPZ	46	39	0				
MVP5180	55	50	59	0			
ANT70	55	50	55	36	0		
VAU	55	51	55	39	36	0	
DUR	56	51	56	39	35	42	0
	LAI	MAL	CPZ	MVP	ANT	VAU	DUR
				5180	70		

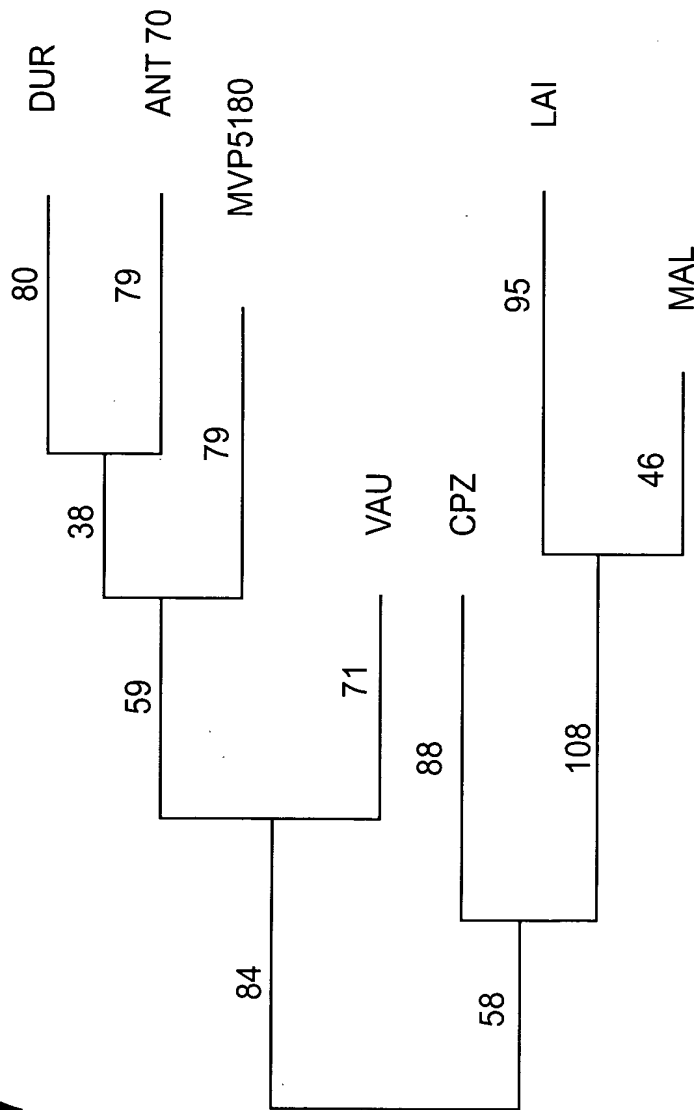
FIG. 16B

GAG (OUT OF 174 AMINO ACIDS)

LAI	0						
MAL	6	0					
CPZ	11	14	0				
MVP5180	21	23	18	0			
ANT70	21	24	19	6	0		
DUR	22	22	19	7	9	0	
	LAI	MAL	CPZ	MVP	ANT	DUR	
				5180	70		

FIG. 16C

FIG. 17



PHYLOGENETIC TREE OF V3
(TREEALIGN PROGRAM, J. HEIN, ON BISANCE, CITI2)
(OUT OF 171 AMINO ACIDS)

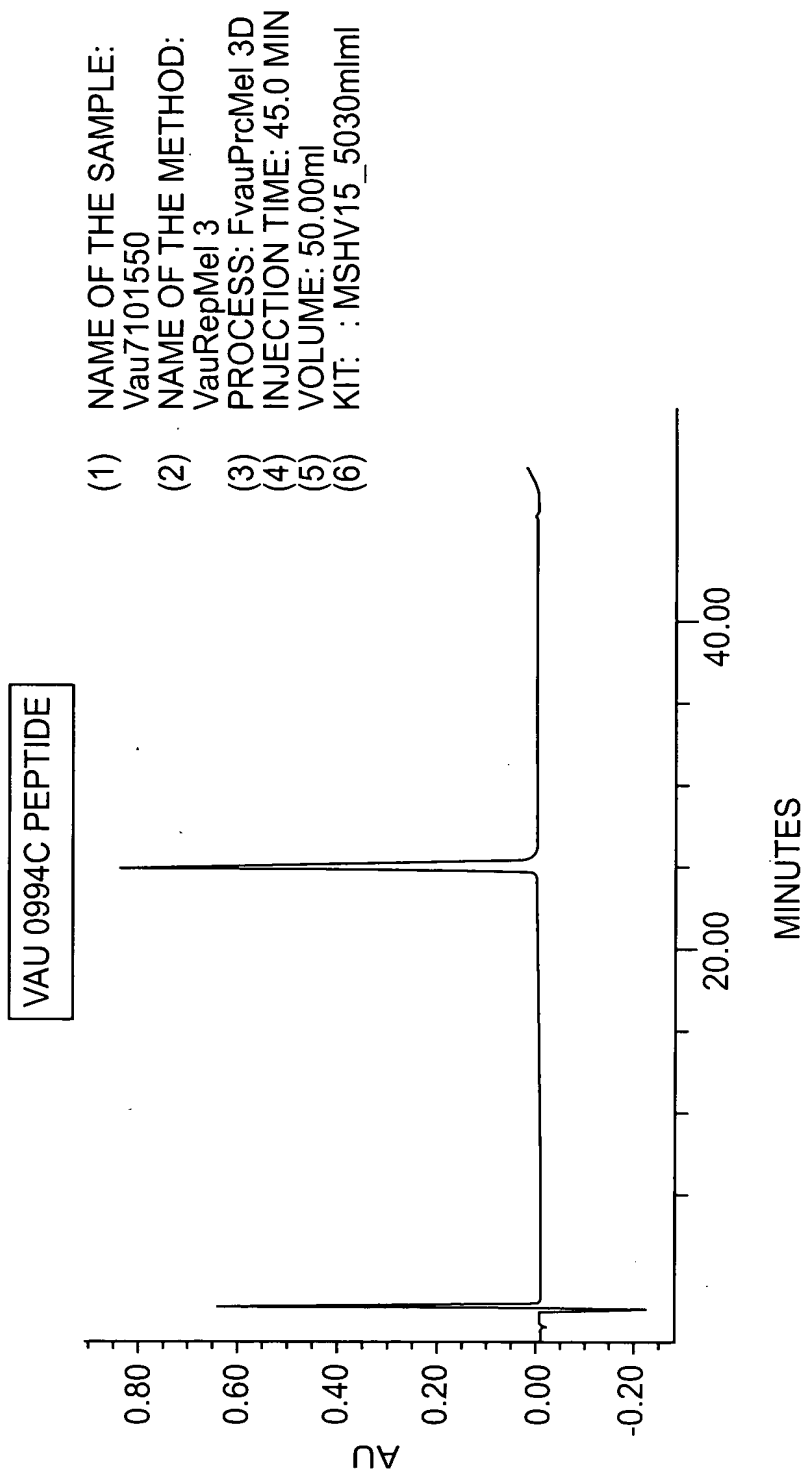
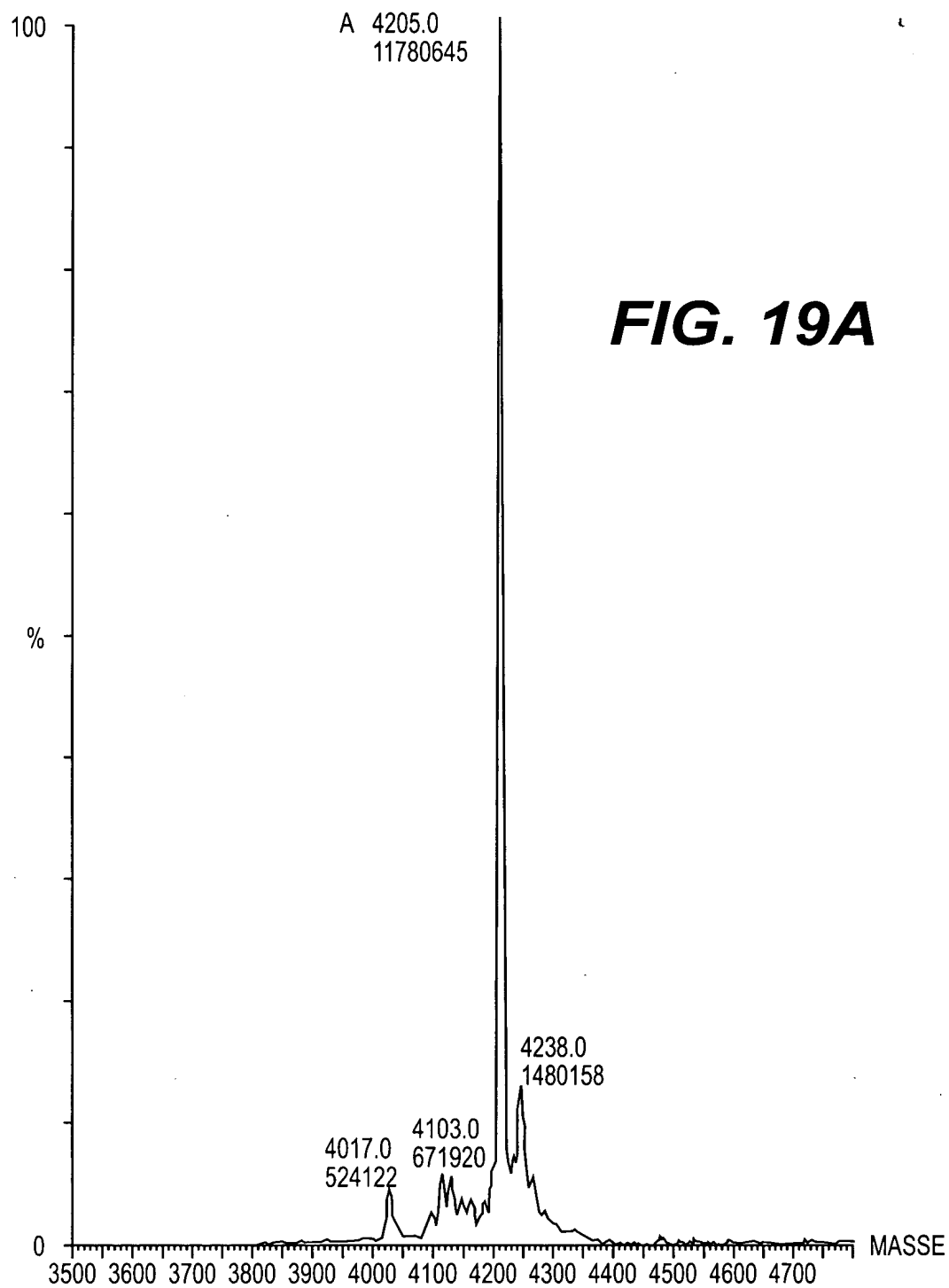


FIG. 18A

CHROMATOGRAPHIC RESULTS

RETENTION TIME (MIN)	INITIAL TIME (MIN)	FINAL TIME (MIN)	% SURFACE AREA	INT TYPE
24.482	23.898	24.932	100.00	BB

FIG. 18B



VAU PEPTIDE

REF: F VAU 0994 C 710

SEQUENCE: RLLALETFIQNQQLLN**WGCKNRLICYTSVKWNKT**

LENGTH: 35

MOLECULAR WEIGHT: 4210

ANALYTICAL CONTROLS: > 95% BY HPLC AND MASS SPECTROMETRY

FIG. 19B

STUDY OF THE IMMUNOREACTIVITY OF THE PEPTIDE
 MIMICKING THE IMMUNODOMINANT EPITOPE OF THE
 GP160 VAU SEQUENCE (SUBTYPE O)

VS=0.1 RATIO	VAU PEPTIDE 2µg/ml
<u>HIV1 SERA (PANEL BBI)</u>	
BO1 NO° 12	0.80
BO1 NO° 13	0.40
BO1 NO° 15	0.80
PRB911K6	0.20
<u>HIV1 SERA (ROMANIA)</u>	
<u>STAGE 3/4</u>	
3989	9.50
5116	8.60
<u>HIV1 SERA (PANEL AFM)</u>	
<u>SUBTYPE O</u>	
MAA	>30
LOB	>30
HAM	>30
DUR	12.50
<u>HIV1 SERUM (REIMS)</u>	
<u>SUB TYPE M?</u>	
MAD	0.20

FIG. 20A

<u>SUSPICION OF SUBTYPE O</u> <u>(YAOUNDE PASTEUR CENTER)</u>	
3372	0.60
3361	>30
1507	28.80
3167	28.70
2628	>30
1060	28.10
4020	0.60
4783	0.30
5322	0.30
6661	0.40
5527	0.50
5863	0.30
5969	25.00
6487	>30
6509	>30
6782	0.70
5453	>30
3826	27.30
<u>HIV2 SERA</u>	1.50
BERT	0.30
PAOL	4.50
RIV	15.80

INDIRECT EIA PROCEDURE; 3 X 30 MIN TYPE GENELAVIA MIXT

FIG. 20B

NEGATIVE SERA	
N=48 AVERAGE	0.022
DS AVERAGE	0.007
+12DS	0.107
VS	0.100

FIG. 20C

SUMMARY OF THE RESULTS OBTAINED ON THE AFRICAN SERA

	WB1 RESULTS									
	GP 160	GP 120	P 68	P 55	GP 41	P 40	P 34	P 25	P 18	
3361	++	+-	+				++	+	+	POS
1507	+	+-					+-	+-		POS
2628	+-		++	++		+	+	++	++	POS
3167	++	+	++	++	+	+	++	++	++	POS
3372	++	+-	+	++	+	+	++	++	+-	POS
5453	++	+-	+	+	+-	+	+	+	+	POS
5863	++	+-	+	+	+-	+-	+	+	+	POS
5969	+--		+	+		+	+	+		IND
6487	++		+	+			+	+-	+-	IND
6782	++		+	+	+	+	+	+		POS
950	+-		+-				+-	+-	+-	IND
1060	+-							+-	+	IND
5527										?
6509	++		+-				+--			IND
6661	+							+		IND
4020= SEMT	+							(+-)		IND
4783= 5322	+-							+-	+-	IND
3826								+-	+-	IND
MAD	++	+	+	+	+	+	+	+	+	POS
DUR										
MAA										
LOB	+		++	+-			++	++		IND
HAM			+				+	+		IND

=RATIO<1
 =RATIO>2

FIG. 21A

TEST DE SCREENING (RATIO : DO/VS)					
		GEM IND HIV1+2	ABBOTT SDW HIV1+2	MUREX SDW HIV1+2	
3361	0.10	18.00	0.56	0.72	1.40
1507	0.97	14.25	3.03	5.35	0.98
2628	0.70	18.00	4.84	1.71	1.34
3167	0.38	18.30	11.89	>6	0.88
3372	0.19	16.80	11.63	3.76	0.47
5453	2.50	>20			1.70
5863	2.30	>20			1.90
5969	2.30	15.20			2.25
6487	0.32	19.70			1.90
6782	0.07	13.40			2.95
950	1.20	6.00	5.76	>6	0.68
1060	0.60	18.00	0.46	1.25	0.67
5527	0.27	2.40			0.52
6509	0.32	>16			2.14
6661	8.10	10.10			1.54
4020= SEMT	0.23	6.30	1.03	4.98	4.12
4783= 5322	0.19	8.10 10.90	0.41		0.55 0.52
3826		3.93		1.64	0.72
MAD	-	+	+		
DUR MAA LOB HAM		>8 >19 >19	2.00 2.00 1.80	0.80 2.70 7.80	 1.50 2.70

FIG. 21B

	EIA PEPTIDES							
	CLONATEC RAP HIV1	39D6 HIV1B	FER HIV1B	39A HIV1B	VAU HIV1O	MVPP 5180 HIV1O	BNR 19 HIV1O	PEPTI- LAV1-2
3361	+				28.8	25.80	NT	
1507	DUBIOUS			8.4	28.7	28.80	1.7	
2628				3.6	28.1	19.30	1.2	
3167	+			>30	>30	>30	1.6	
3372	+/-			2.8	>30	24.00	4.9	
5453	-	4.36	1.37	3.6	27.3		1.6	-
5863	-	1.42	0.40	1.4	25		0.5	-
5969	-	0.94	1.90	19.4	>30		0.6	+
6487	+	25.75	5.76	>30	>30		0.7	
6782	-	0.64	0.49	0.8	>30		10.3	-
950					0.6		0.4	
1060	DUBIOUS			1.9	0.6	0.40	0.6	
5527	-			4.5	0.3		0.2	+/-
6509	+			16.9	0.7		0.2	
6661	+			2.8	0.5		0.4	
4020=	?Ag-			1.15	0.3		0.5	
SEMT				1.2	0.7		0.9	
4783=				2.5	0.3		0.3	
5322				4	0.4		0.3	
3826				1.6	1.5		0.7	
MAD		0.66	2.72	26.7	0.2		>30	-
DUR		>30	>30	>30	12.5		0.2	
MAA				NT	>30		NT	
LOB		1.02	5.62	12.5	>30		>30	
HAM		0.73	0.41	13.3	>30		0.7	

FIG. 21C